SEQUENCE LISTING

	110> Pfizer Inc. Harland, Lee						
<120>	Novel Polypeptide						
<130>	> PC10970AGLK						
<150> <151>							
<150> <151 _{>}	US 60/267,341 2001-02-08						
<160>	3						
<170>	PatentIn version 3.1						
<210><211><211><212><213>	1 918 DNA Homo	sapiens					
<400> atgccto	1 ggcc	acaatacctc	caggaattcc	tcttgcgatc	ctatagtgac	accccactta	60
atcagco	ctct	acttcatagt	gcttattggc	gggctggtgg	gtgtcatttc	cattcttttc	120
ctcctgg	gtga	aaatgaacac	ccggtcagtg	accaccatgg	cggtcattaa	cttggtggtg	180
gtccaca	agcg	tttttctgct	gacagtgcca	tttcgcttga	cctacctcat	caagaagact	240
tggatgt	ttg	ggatgacatt	ctgcaaattt	gtgagtgcca	tgctgcacat	ccacatgtac	300
ctcacgt	tcc	tattctatgt	ggtgatcctg	gtcaccagat	acctcatctt	cttcaagtgc	360
aaagaca	aaag	tggaattcta	cagaaaactg	catgctgtgg	ctgccagtgc	tggcatgtgg	420
acgctgg	gtga	ttgtcattgt	ggtacccctg	gttgtctccc	ggtatggaat	ccatgaggaa	480
tacaat	gagg	agcactgttt	taaatttcac	aaagagcttg	cttacacata	tgtgaaaatc	540
atcaact	tata	tgatagtcat	ttttgtcata	gccgttgctg	tgattctgtt	ggtcttccag	600
gtcttca	atca	ttatgttgat	ggtgcagaag	ctacgccact	ctttactatc	ccaccaggag	660
ttctggg	gctc	agctgaaaaa	cctattttt	ataggggtca	tecttgtttg	tttccttccc	720
taccagt	tct	ttaggatcta	ttacttgaat	gttgtgacgc	attccaatgc	ctgtaacagc	780
aaggtt	gcat	tttataacga	aatcttcttg	agtgtaacag	caattagctg	ctatgatttg	840
cttctct	ttg	tctttggggg	aagccattgg	tttaagcaaa	agataattgg	cttatggaat	900
tgtgttt	tgt	gccgttag					918

<210> 2

<211> 305

<212> PRT

<213> Homo sapiens

<400> 2

Met Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val 1 5 10 15

Thr Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu 20 25 30

Val Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg

Ser Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val 50 55 60

Phe Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr 65 70 75 80

Trp Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His 85 90 95

Ile His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr

Arg Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg

Lys Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile 130 135 140

Tyr Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr 165 170 175

Tyr Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val 180 185 190

Ala Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val

195 200 205

Gln Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln 210 215 220

Leu Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro 225 230 235 240

Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn 245 250 255

Ala Cys Asn Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val 260 265 270

Thr Ala Ile Ser Cys Tyr Asp Leu Leu Phe Val Phe Gly Gly Ser 275 280 285

His Trp Phe Lys Gln Lys Ile Ile Gly Leu Trp Asn Cys Val Leu Cys 290 295 300

Arg

<210> 3

<211> 337

<212> PRT

<213> Homo sapiens

<400> 3

Met Asp Glu Thr Gly Asn Leu Thr Val Ser Ser Ala Thr Cys His Asp 1 5 10 15

Thr Ile Asp Asp Phe Arg Asn Gln Val Tyr Ser Thr Leu Tyr Ser Met 20 25 30

Ile Ser Val Val Gly Phe Phe Gly Asn Gly Phe Val Leu Tyr Val Leu $35 \hspace{1cm} 40 \hspace{1cm} 45 \hspace{1cm}$

Ile Lys Thr Tyr His Lys Lys Ser Ala Phe Gln Val Tyr Met Ile Asn 50 60

Leu Ala Val Ala Asp Leu Leu Cys Val Cys Thr Leu Pro Leu Arg Val 65 70 75 80

Val Tyr Tyr Val His Lys Gly Ile Trp Leu Phe Gly Asp Phe Leu Cys 85 90 95

Arg Leu Ser Thr Tyr Ala Leu Tyr Val Asn Leu Tyr Cys Ser Ile Phe 100 105 110

Phe Met Thr Ala Met Ser Phe Phe Arg Cys Ile Ala Ile Val Phe Pro 115 120 125

Val Gln Asn Ile Asn Leu Val Thr Gln Lys Lys Ala Arg Phe Val Cys 130 135 140

Val Gly Ile Trp Ile Phe Val Ile Leu Thr Ser Ser Pro Phe Leu Met 145 150 155 160

Ala Lys Pro Gln Lys Asp Glu Lys Asn Asn Thr Lys Cys Phe Glu Pro 165 170 175

Pro Gln Asp Asn Gln Thr Lys Asn His Val Leu Val Leu His Tyr Val 180 185 190

Ser Leu Phe Val Gly Phe Ile Ile Pro Phe Val Ile Ile Ile Val Cys 195 200 205

Tyr Thr Met Ile Ile Leu Thr Leu Leu Lys Lys Ser Met Lys Lys Asn 210 215 220

Leu Ser Ser His Lys Lys Ala Ile Gly Met Ile Met Val Val Thr Ala 225 230 235 240

Ala Phe Leu Val Ser Phe Met Pro Tyr His Ile Gln Arg Thr Ile His 245 250 255

Leu His Phe Leu His Asn Glu Thr Lys Pro Cys Asp Ser Val Leu Arg 260 265 270

Met Gln Lys Ser Val Val Ile Thr Leu Ser Leu Ala Ala Ser Asn Cys 275 280 285

Cys Phe Asp Pro Leu Leu Tyr Phe Phe Ser Gly Gly Asn Phe Arg Lys 290 295 300 Arg Leu Ser Thr Phe Arg Lys His Ser Leu Ser Ser Val Thr Tyr Val 305 310 310 315 320

Pro Arg Lys Lys Ala Ser Leu Pro Glu Lys Gly Glu Glu Ile Cys Lys 325 330 335

Val